

Figure 1

Subtracting homogenized  $A^{+++}$  according to the introduced method of subtraction



Constructing several homogenized sublibraries with  $C_0t \leq 1$  so that the highly expressed cDNAs in A, B, C.....can be enriched in the column, and those in elution peak are the high abundance cDNAs that only express in A. They are designated as:  $spA_1^{+++}$ .  $spA_2^{+++}$ .....



Similarly, homogenizing library  $A^{++}$  with  $1 \leq C_0t \leq 50$  so that homogenized sublibraries that contains the moderate abundance cDNA only expressed in A can be obtained in elution peak. They are designated as:  $spA_1^{++}$ .  $spA_2^{++}$ .....



Similarly, homogenizing library  $A^{+}$  when  $C_0t \geq 1-50$  so that homogenized libraries that contains the low abundance or rare cDNA only expressed in A can be obtained in elution peak. They are designated as:  $spA_1^{+}$ .  $spA_2^{+}$ .....

Figure 2

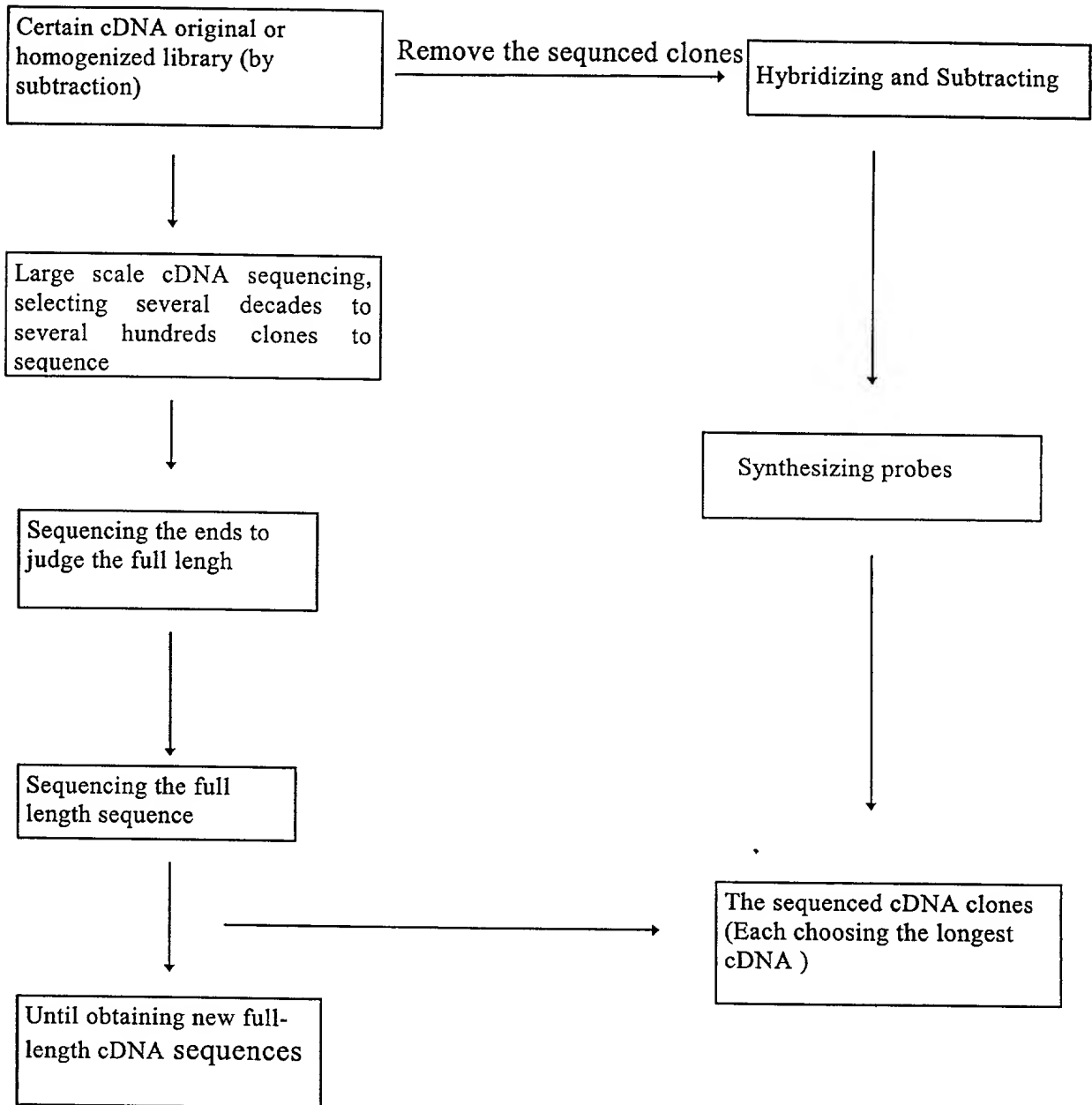


Figure 3